

Fig. 1

Fig. 2

Codon	AA	MSP wt	Edited MSP	MSP wt	Edited MSP	E. coli	Human
TTT	Phe	8	0	0.53	0	0.5	0.35
TTC	Phe	7	15	0.47	1	0.5	0.65
TTA	Leu	25	0	0.66	0	0.11	0.05
TTG	Leu	3	0	0.08	0	0.11	0.09
TCT	Ser	4	1	0.17	0.04	0.27	0.17
TCC	Ser	2	3	0.09	0.13	0.21	0.26
TCA	Ser	10	1	0.43	0.04	0.13	0.11
TCG	Ser	0	0	0	0	0.14	0.07
TAT	Tyr	17	2	0.85	0.1	0.54	0.47
TAC	Tyr	3	18	0.15	0.9	0.46	0.53
TAA	...	0	0	0	0	0	0
TAG	...	0	0	0	0	0	0
TGT	Cys	10	12	0.83	1	0.45	0.3
TGC	Cys	2	6	0.17	0	0.55	0.7
TGA	...	0	0	0	0	0	0
TGG	Trp	0	0	0	0	0	1
CTT	Leu	9	0	0.24	0	0.12	0.11
CTC	Leu	0	0	0	0	0.12	0.22
CTA	Leu	1	0	0.02	0	0.03	0.07
CTG	Leu	0	38	0	0	0.72	0.46
CCT	Pro	4	2	0.4	0.2	0.14	0.24
CCC	Pro	1	6	0.1	0.6	0.11	0.51
GCA	Pro	5	1	0.5	0.1	0.2	0.24
CGG	Pro	0	0	0	0.1	0.54	0.11
GAT	His	3	1	0.75	0	0.64	0.42
GAC	His	1	4	0.25	1	0.36	0.58
GAA	Gln	9	0	1	0	0.31	0.26
GAG	Gln	0	9	0	1	0.69	0.74
GGT	Arg	1	0	0.17	0	0.46	0.09
GGA	Arg	0	0	0	0	0.32	0.19
GGG	Arg	1	0	0.17	0	0.05	0.1
ATT	Ile	13	0	0.65	0	0.06	0.15
ATA	Ile	2	20	0.11	0	0.39	0.23
ATG	Ile	3	0	0.25	0	0.08	0.13
ACT	Met	3	3	1	1	1	1
ACC	Thr	3	2	0.19	0.13	0.36	0.2
ACA	Thr	3	13	0.19	0.81	0.38	0.47
ACG	Thr	9	1	0.56	0.06	0.09	0.21
ACG	Thr	1	0	0.06	0	0.17	0.12
AAT	Asn	29	3	0.71	0.07	0.29	0.14
AAC	Asn	12	38	0.29	0.93	0.71	0.66
AAA	Lys	38	0	0.9	0	0.72	0.45
AAG	Lys	4	42	0.1	0.1	0.28	0.55
AGT	Ser	5	2	0.21	0.09	0.11	0.11
AGC	Ser	2	16	0.09	0.7	0.14	0.29
AGA	Arg	4	3	0.57	0.5	0.08	0.24
AGG	Arg	0	0	0	0	0.03	0.23
GTT	Val	15	0	0.71	0	0.37	0.13
GTC	Val	1	11	0.05	0.52	0.12	0.27
GTA	Val	5	0	0.24	0	0.28	0.09
GTG	Val	0	10	0	0.48	0.23	0.5
GCT	Ala	2	0	0.22	0	0.33	0.11
GCC	Ala	1	8	0.11	0.89	0.18	0.4
GCA	Ala	6	1	0.62	0.11	0.28	0.17
GCG	Ala	0	0	0	0	0.21	0.12
GAT	Asp	25	27	0.93	0	0.48	0.36
GAC	Asp	2	0	0.07	0	0.52	0.62
GAA	Glu	21	3	0.84	0.12	0.67	0.4
GAG	Glu	4	22	0.16	0.88	0.33	0.6
GGT	Gly	8	4	0.57	0.29	0.46	0.15
GGA	Gly	0	0	0	0	0.4	0.44
GGA	Gly	6	3	0.43	0.21	0.05	0.17
GGG	Gly	0	7	0	0.5	0.08	0.24

Fig. 3b

Codon	AA	gb-casein	sh-casein	MSP wt	Edited MSP	mouse b-casein	mouse s-casein	mouse g-casein	mouse e-casein
TTT	Phe	5	4	4	0	4	8	3	4
TTC	Phe	4	3	7	15	4	6	7	1
TTA	Leu	0	2	25	0	0	0	0	0
TTG	Leu	0	2	3	0	0	0	0	0
TCT	Ser	5	1	4	1	13	0	7	5
TCC	Ser	2	2	2	3	6	14	8	2
TCA	Ser	1	4	10	1	1	3	2	0
TCG	Ser	0	1	0	0	0	0	2	0
TAT	Tyr	2	7	17	2	1	3	2	0
TAC	Tyr	1	2	3	18	2	6	6	7
TAA	...	0	0	0	0	1	0	1	0
TAG	...	0	0	0	0	0	0	0	0
TGT	Cys	1	1	10	12	0	0	0	0
TGC	Cys	0	2	2	0	2	2	1	0
TGA	...	0	0	0	0	0	1	0	1
TGG	Trp	1	1	0	0	0	2	2	2
CTT	Leu	9	1	9	0	16	9	3	3
CTC	Leu	5	2	0	0	7	8	0	1
CTA	Leu	1	2	1	0	1	2	4	0
CTG	Leu	11	5	0	38	10	17	4	0
CCT	Pro	17	6	4	2	8	6	3	0
CCC	Pro	12	0	1	6	8	6	2	0
GCA	Pro	3	13	5	1	5	6	6	4
CGG	Pro	1	1	0	1	0	0	0	2
GAT	His	0	1	3	0	2	6	0	1
GAC	His	5	3	1	4	4	21	3	7
GAA	Gln	16	6	0	9	21	32	12	8
GAG	Gln	0	1	1	0	0	0	0	0
GGT	Arg	0	0	0	0	1	0	0	0
GGA	Arg	1	0	0	0	0	0	0	0
GGG	Arg	0	0	0	0	0	0	0	0
ATT	Ile	6	3	2	20	7	5	3	4
ATA	Ile	1	3	5	0	1	12	2	0
ATG	Met	7	3	3	3	4	5	1	13
ACT	Thr	2	6	3	2	6	4	1	4
ACC	Thr	2	7	3	13	4	4	4	4
ACA	Thr	2	4	9	1	1	2	2	0
ACG	Thr	0	0	1	0	0	0	2	0
AAT	Asn	2	6	29	3	4	6	3	1
AAC	Asn	2	3	12	38	4	9	4	6
AAA	Lys	7	6	38	0	6	7	3	5
AAG	Lys	6	4	4	42	3	6	6	7
AGT	Ser	2	6	5	2	3	6	5	6
AGC	Ser	5	0	2	16	3	8	6	3
AGA	Arg	2	2	4	3	0	0	1	1
AGG	Arg	0	2	0	0	0	0	0	0
GTT	Val	8	5	15	0	7	4	2	3
GTC	Val	2	1	11	0	7	3	3	0
GTA	Val	2	2	5	0	2	4	1	3
GTG	Val	8	4	0	10	6	3	5	2
GCT	Ala	1	3	2	0	8	17	4	2
GCC	Ala	4	7	1	8	6	3	3	3
GCA	Ala	3	7	6	1	4	13	1	1
GCG	Ala	0	1	0	0	0	0	0	0
GAT	Asp	4	5	25	27	3	6	4	2
GAC	Asp	0	2	2	0	1	1	1	3
GAA	Glu	10	6	21	3	6	12	5	8
GAG	Glu	9	5	4	22	5	5	3	5
GGT	Gly	2	1	8	4	0	0	0	0
GGA	Gly	0	0	0	0	0	0	0	0
GGA	Gly	2	1	6	3	1	0	0	0
GGG	Gly	1	0	0	0	7	1	0	0

Fig. 3a

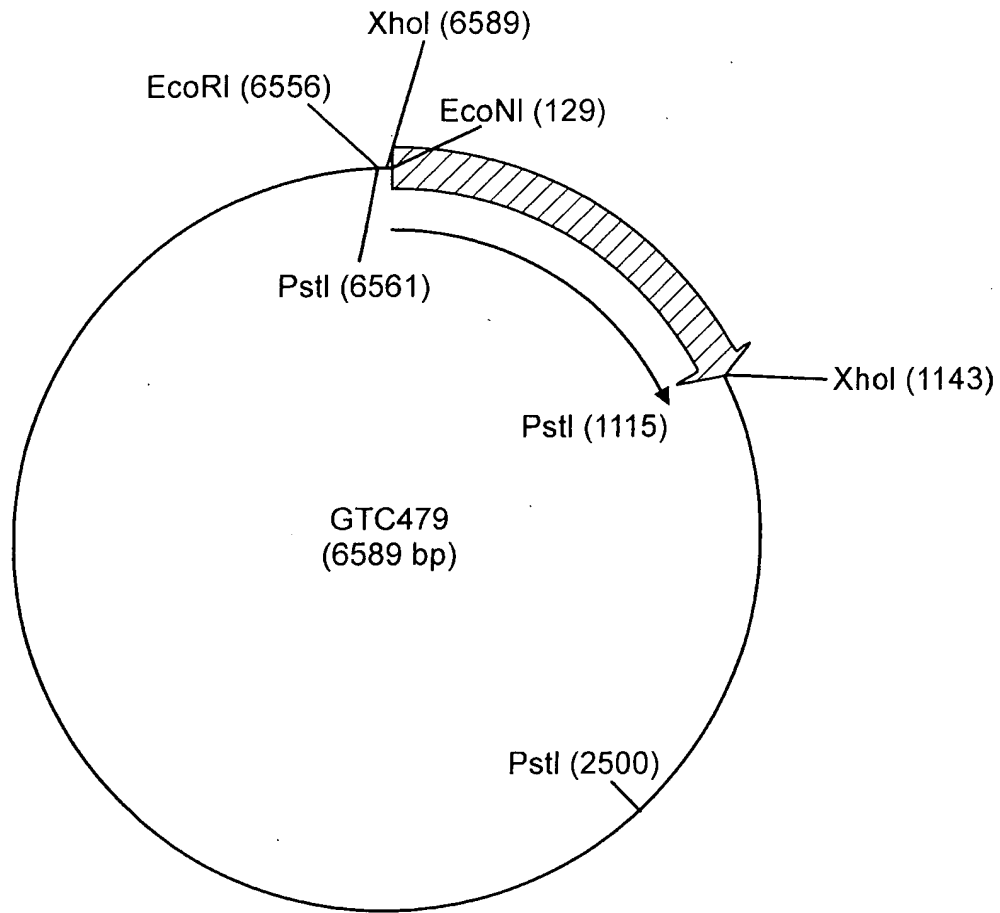


FIG. 4A

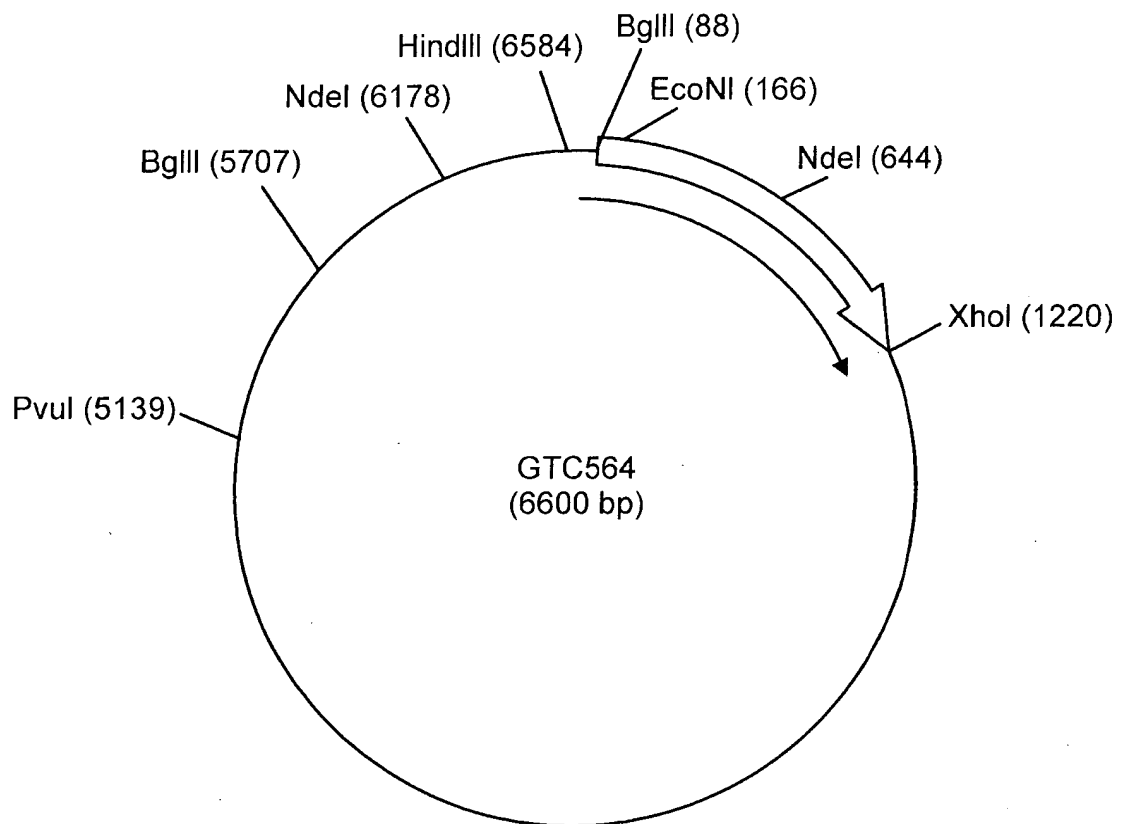


FIG. 4B

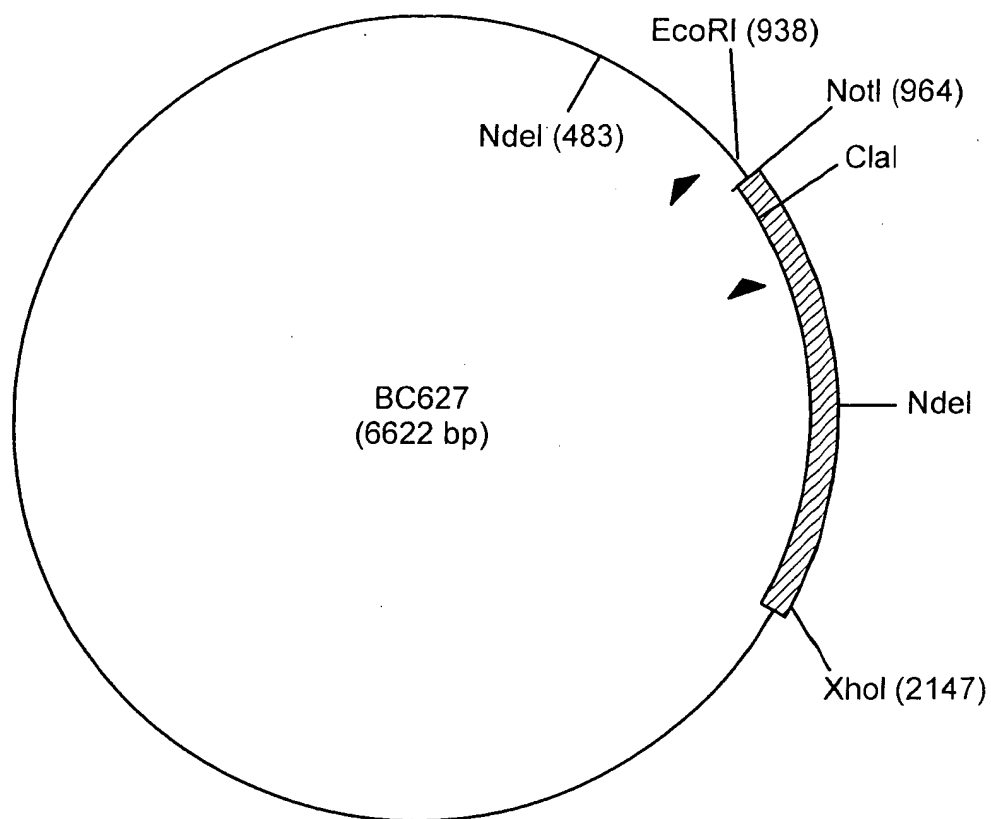


FIG. 4C

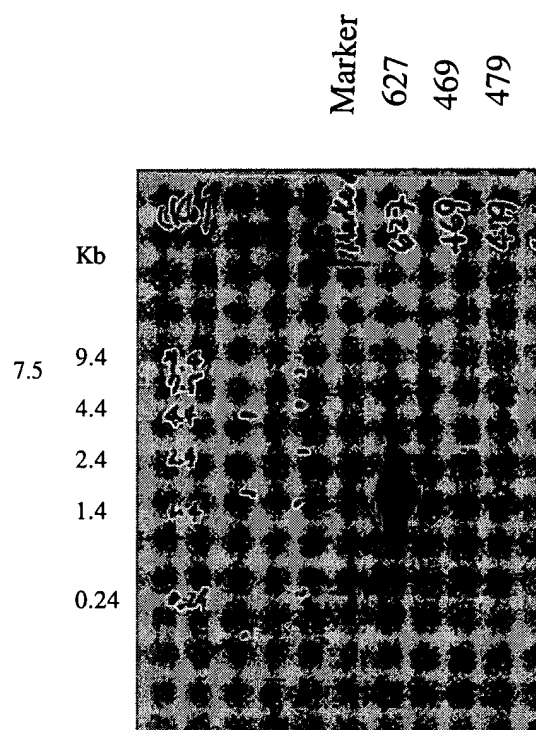


Fig. 5 Panel A

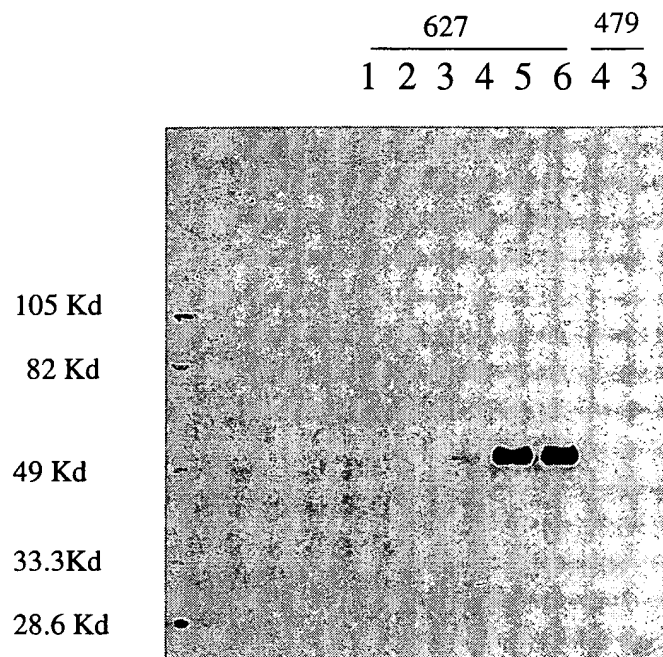


Fig. 5 Panel B

Oligos used:

Sequence ID NO. 3:
TCG ACG AGA GCC ATG AAG GTC CTC ATC CTT GCC TGT CTG GTG GCT
CTG GCC ATT GCA AGA GAG CAG GAA GAA CTC AAT GTA GTC GGT A,

Sequence ID NO. 4:
GAT CTA CCG ACT ACA TTG AGT TCT TCC TGC TCT CTT GCA ATG GCC
AGA GCC ACC AGA CAG GCA AGG ATG AGG ACC TTC ATG GCT CTC G,

Sequence ID NO. 5:
AATAGATCTGCAGTAACTCCTTCCGTAATTG,

Sequence ID NO. 6:
AATTCTCGAGTTAGTGGTGGTGGTGACTGCAGAAATACCATC

Sequence ID NO. J:
TAACTCGAGCGAACCATGAAGGTCCCTCATCCTTGCTGTGGTGGCTCTGG
CCATTGCA

FIG. 6

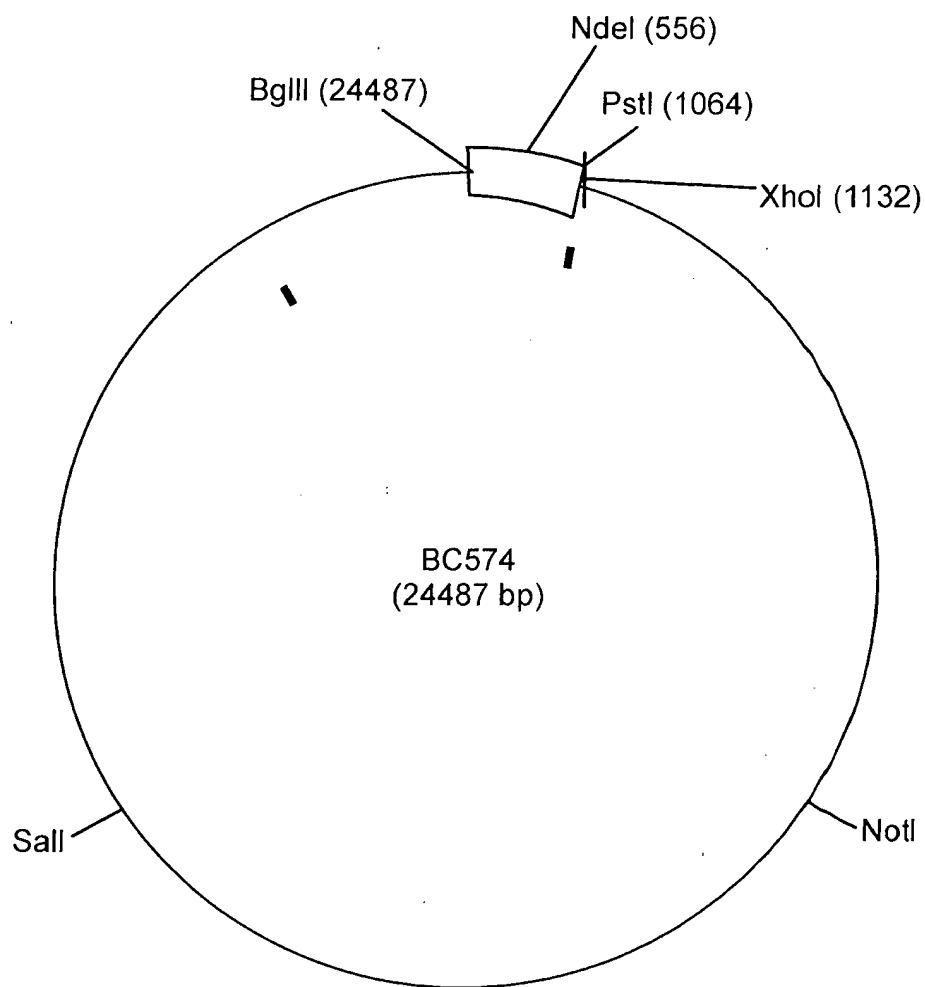


FIG. 7

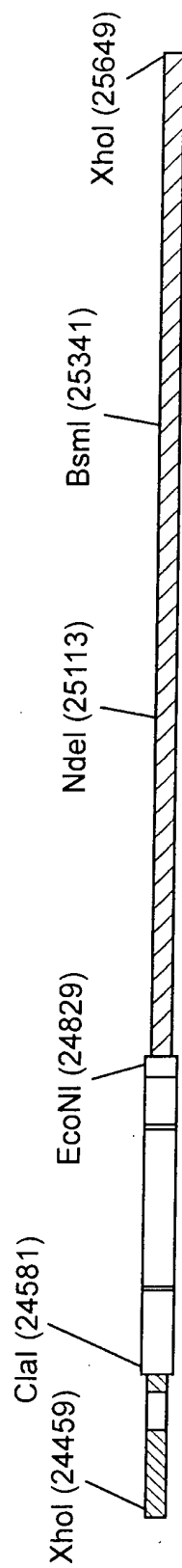


Diagram of BC620

FIG. 8

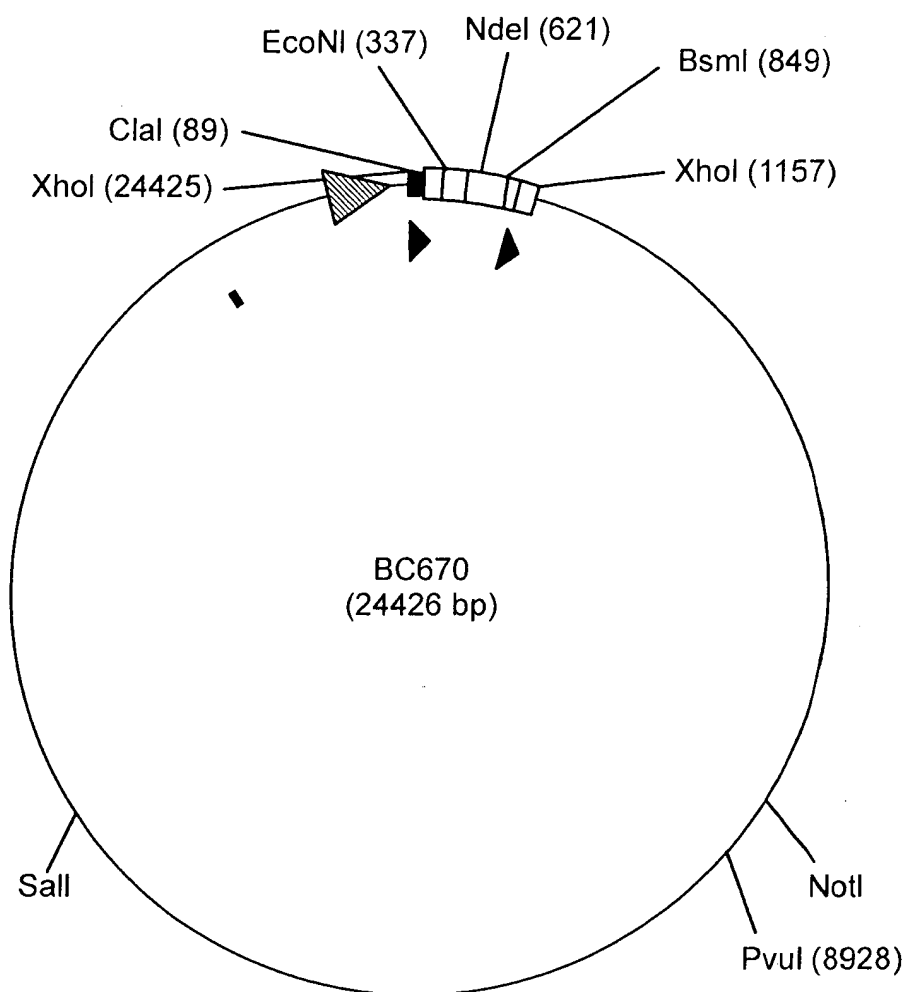


FIG. 9

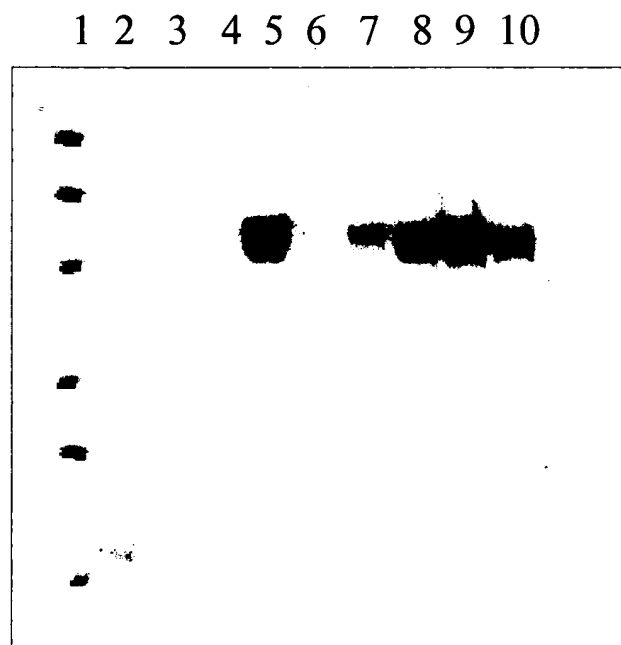


Fig. 10

26 CATGAAGGTCTCATAATTCCTGTCTGTGGCTCTGGCCATTGCGCCGTCACCTCCCTCGTCATCGATAA
1▶ M K V L I A C L V A L A I A A V T P S V I D N
98 CATCTGTCCAAGATCGAAGACGAGTACGAGGTGCTGTACTCTGAAGCCCTGCCAGGAGTCTACAGGAGCC
24▶ I L S K I E N E Y E V L Y L K P L A G V Y R S
169 TGAAGAAGCAGCTGGAGCAACAACCTGATGACCTCAACCTGAACCTGAAGGATATCTGAAACAGCAGGTTCA
48▶ L K K Q L E N N V M T F N V N V K D I L N S R F
241 ACAAGAGGGAGAAGTCAAGAACCTGTGGAGAGCGATCTGATCCCTTACAAGGATCTGACCGAGCAACT
72▶ N K R E N F K N V L E S D L I P Y K D L T S S N
313 ACGTGGTCAAAGAT EcoNI (337) AAGAGAGATAAGTTCTCTGAGCAGTTACAAATTACA
96▶ V V K D P Y K F L N K E K R D K F L S S Y N Y
385 TCAAGGATAGCATTGACACCGGATCAACTTCGCCAACGATGCTCTGGGATCTACTACAAGATCCTGTCTCGAGA
120▶ I K D S I D T D I N F A N D V L G Y Y K I L S E
457 AGTACAAGCGGATCTGGATAGCATCAAGAAAGTACATCAACGATAAGCAGGAGAGAGAACGAGAGTACCTGC
144▶ K Y K S D L D S I K K Y I N D K Q G E N E K Y L
529 CCTCTGAAACATCGAGACCTGTACAAGACCTCAACGATAAGATTGATCTGTCTGATCCACCTGG
168▶ P F L N N I E T L Y K T V N D K I D L F V I H L
601 AGGCCAAG CAG A AGAGCAACGTGGAGGTCAAGATCAAGGAGCTGAATTACCTGA
192▶ E A K V L Q Y T Y E K S N V E V K I K E L N Y L
673 AGACCATCCAGGATAAGCTGGCCGATTTCAGAGAGAACACACACTTCGTGCGGAATCGCCGATCTGAGACCG
216▶ K T I Q D K L A D F K K N N N F V G I A D L S T
745 ATTACAACCAACAACCTCTGACCAAGTCTCTGAGCACCAGGAAATGGTCTTCGAAACCTGGCCCAAGACCG
240▶ D Y N H N N L L T K F L S T G M V F E N L A K T
817 TCCTGAGCAACCTGCTGGATGGAAACCTG BsmI (849) CAG CAGCACCAGTGTGTGAAGAAG
264▶ V L S N L L D G N L Q G M L Q I S Q H Q C V K K
888 CAGTGTCCCCAGACAGCGGATGCTTCAGACACCTGGATGAGGAGGAGGAGTGCAGAGTGCCTGCTGAAGT
288▶ Q C P Q N S G C F R H L D E R E E C K C L L N
958 ACAAGCAGGAAGGAGATAAGTGTGTGGAACCCCACTCTTGTAAACGAGACAAATGGAGGATGCCAT
311▶ Y K Q E G D K C V E N P N P T C N E N N G C D
1029 GCCGATGCCAAGTCTACCGAGGAGGATTCAGGAAGCAACGAAAGAGATCACTGCGAGGTGTACCAAGCC
335▶ A D A K C T E E D S G S N G K I T C E C T K P XhoI (1157)
1100 TGATTCTTATCCACTGTTCGATGGATTTCTGTGAGTCACCAACCACCACCACTAACTCGAGGATCC
358▶ D S Y P L F D G I F C S H H H H H L E D

Fig. 11

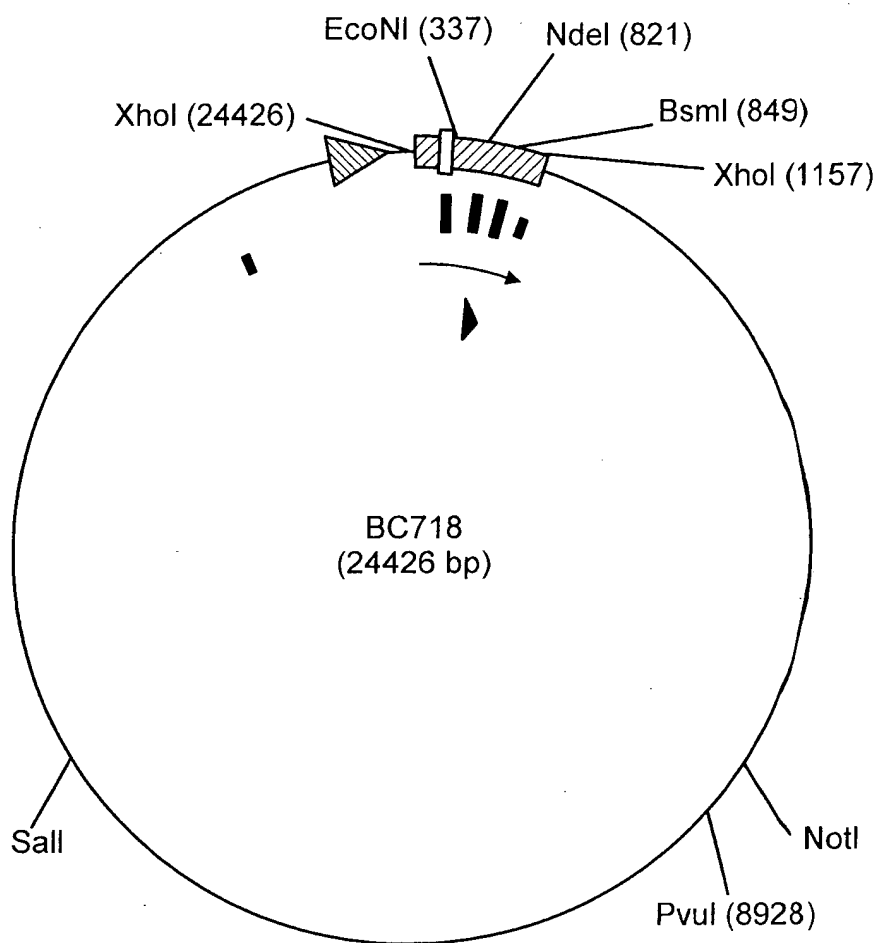


FIG. 12

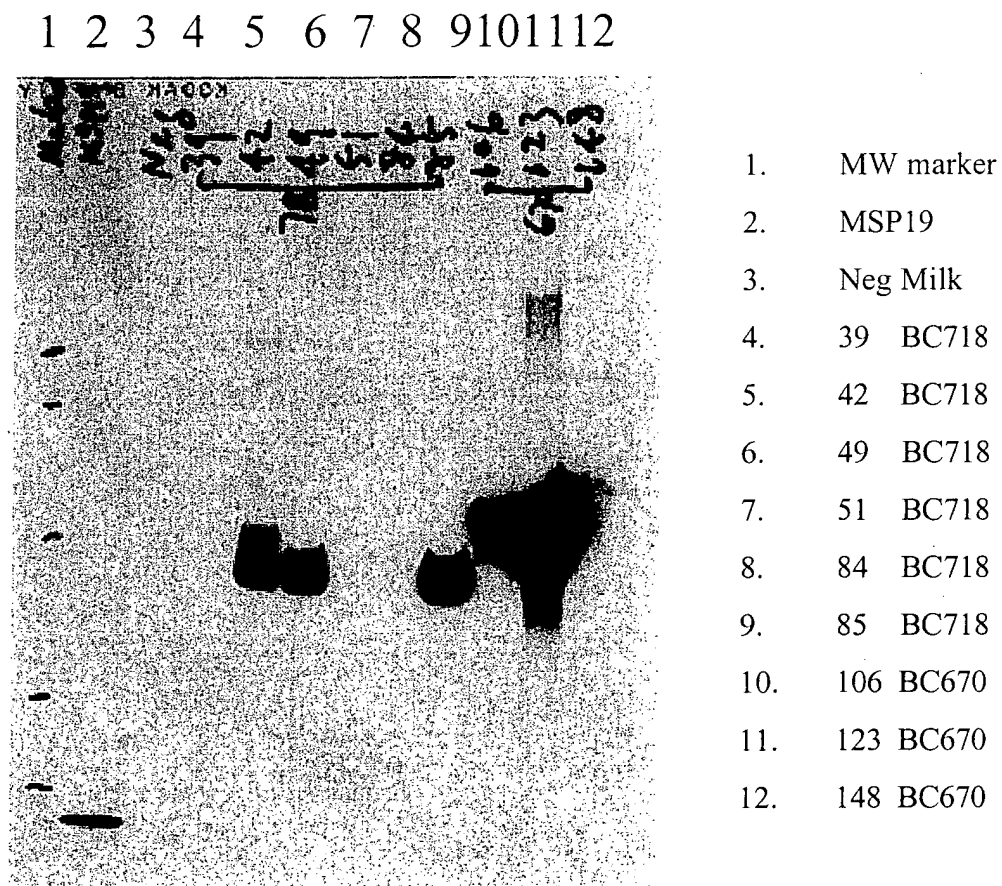


Fig. 13